

10 / 583785

## VIERING, JENTSCHURA & PARTNER



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JUN 2005

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Ihr Zeichen/Your ref.: Unser Zeichen/Our file: Bearbeiter: Datum/Date:  
**P23795**                   **Sd/Ws**                   **18.03.2004**

**International Patent Application PCT/EP03/14542  
"Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use"  
Appl.: Prof. Dr. Werner Seeger**

In reply to the Communication dated February 20, 2004.

an amended sequence listing is filed herewith in written form as well as in computer-readable from (ASCII format; file name: 23795\_seq.txt) saved on the enclosed diskette.

The amended sequence listing does not go beyond the disclosure in the application as filed. It now includes the pure amino acid sequences of SEQ ID NOs 1 to 13, which are referred to as SEQ ID NOs 14 to 26, respectively.

Encl.  
Sequence listing, paper copy  
Diskette

# Hans-Martin Viering

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AP20 Rec'd PCT/PTO 19 JUN 2006

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger

<120> Novel chimeric plasminogen activators and their pharmaceutical use

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

48

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

96

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag  
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

144

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

192

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac  
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

240

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg  
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

288

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc  
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

336

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag  
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

384

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa  
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

432

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg  
Ser Arg Gln Pro Glu Pro Gln Glu Pro Gly Met Ser Asp Pro Leu  
145 150 155 160

480

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc

528

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu			
165	170	175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac			576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His			
180	185	190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc			624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195	200	205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag			672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg			720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc			768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc			816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260	265	270	
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg			864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro			
275	280	285	
aca gga gaa tgg ctg ccc cga gac tct gag tgc cac ctc tgc atg tcc			912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser			
290	295	300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca			960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala			
305	310	315	320
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag			1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys			
325	330	335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg			1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg			
340	345	350	
ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc			1104
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr			
355	360	365	
atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt			1143
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu			
370	375	380	

<210> 2  
<211> 837  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<400> 2

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1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	96
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	144
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	192
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	240
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	288
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	336
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	384
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	432
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Gln Glu Pro Gly Met Ser Asp Pro Leu	480
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	528
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	576
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195	200	205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag			672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg			720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc			768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc			816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260	265	270	
ctc gtc ctc cgg tgc tcc atg			837
Leu Val Leu Arg Cys Ser Met			
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<210> 3

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (237)

<223> Coding sequence of the mature surfactant protein B

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1	5	10	15

cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc			96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala			
20	25	30	

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc			144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys			
35	40	45	

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc			192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg			
50	55	60	

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg			237
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<210> 4

<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

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Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
   1           5           10          15

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gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac 96  
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
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tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144  
 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
           35                  40                  45

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192  
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
       50             55             60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240  
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
   65               70               75               80

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aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct      288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
          85           90           95

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gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt      336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
          100           105           110

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cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg 384  
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
                  115             120             125

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa 432  
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
     130                135                140

gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct 480  
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
 145 150 155 160

cca gaa gaa tta aaa tt cag tgt ggc caa aag act ctg agg ccc cgc 528  
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
 165 170 175

ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg . 576  
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp  
180 185 190

ttt gcg gcc atc tac agg agg cac cg<sub>g</sub> ggg ggc tct gtc acc acc tac gtg 624

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val			
195	200	205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac			672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His			
210	215	220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt			720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly			
225	230	235	240
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg			768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val			
245	250	255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac			816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His			
260	265	270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt			864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys			
275	280	285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat			912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr			
290	295	300	
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa			960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys			
305	310	315	320
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt			1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val			
325	330	335	
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Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly			
340	345	350	
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa			1104
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
355	360	365	
aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc			1152
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
370	375	380	
caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt			1200
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys			
385	390	395	400
gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta			1248
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu			
405	410	415	
ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc			1293
Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu			
420	425	430	

<210> 5  
<211> 828  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (828)  
<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

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1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	96
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	144
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	192
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	240
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	288
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	336
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	384
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	432
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	480
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	528
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576

Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln			
180	185	190	
ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct			624
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala			
195	200	205	
gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc			672
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro			
210	215	220	
ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc			720
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser			
225	230	235	240
tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga			768
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg			
245	250	255	
gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat			816
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn			
260	265	270	
ggc ctg gcc ctc			828
Gly Leu Ala Leu			
275			
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<b>&lt;211&gt; 1671</b>			
<b>&lt;212&gt; DNA</b>			
<b>&lt;213&gt; Artificial Sequence</b>			
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<b>&lt;221&gt; CDS</b>			
<b>&lt;222&gt; (1) ... (837)</b>			
<b>&lt;223&gt; Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide</b>			
 <b>&lt;220&gt;</b>			
<b>&lt;221&gt; CDS</b>			
<b>&lt;222&gt; (844) ... (1671)</b>			
<b>&lt;223&gt; Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator</b>			
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atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg			48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr			
1	5	10	15
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt			96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys			
20	25	30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag			144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln			
35	40	45	

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Glu Val Trp Gly His Val Gly	50	55	60	192
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	65	70	75	240
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	85	90	95	288
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	100	105	110	336
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	115	120	125	384
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	130	135	140	432
tcc cgg cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	145	150	155	480
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	165	170	175	528
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	180	185	190	576
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	195	200	205	624
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	210	215	220	672
ggg gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	225	230	235	720
gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	245	250	255	768
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	260	265	270	816
ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu	275	280	285	864

gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys 290 295 300	912
att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala 305 310 315 320	960
gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly 325 330 335	1008
ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe 340 345 350	1056
att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser 355 360 365	1104
agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn 370 375 380	1152
ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn .385 390 395 400	1200
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag Asp Ile Ala Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln 405 410 415	1248
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp 420 425 430	1296
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn 435 440 445	1344
tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys 450 455 460	1392
ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu 465 470 475 480	1440
gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp 485 490 495	1488
tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly 500 505 510	1536
cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu	1584

515

520

525

aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg  
 Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp  
 530 535 540

atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc  
 Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
 545 550 555

<210> 7  
 <211> 1674  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1) ... (837)  
 <223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>  
 <221> CDS  
 <222> (847) ... (1674)  
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 7

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg  
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
 1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
 50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
 65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg  
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
 85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc  
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
 100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag  
 384

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln			
115	120	125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa			432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys			
130	135	140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg			480
Ser Arg Gln Pro Glu Pro Gln Glu Pro Gly Met Ser Asp Pro Leu			
145	150	155	160
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc			528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu			
165	170	175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac			576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His			
180	185	190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc			624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195	200	205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag			672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggc gca gtc gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg			720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc			768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc			816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260	265	270	
ctc gtc ctc cgg tgc tcc atg cag ata tct aag ccc tcc tct cct cca			864
Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro			
275	280	285	
gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt			912
Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe			
290	295	300	
aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt			960
Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe			
305	310	315	320
gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt			1008
Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys			
325	330	335	
gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc			1056
Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys			
340	345	350	

ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg 355	360	365	1104
tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu 370	375	380	1152
aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His 385	390	395	1200
aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala 405	410	415	1248
cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn 420	425	430	1296
gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu 435	440	445	1344
aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val 450	455	460	1392
aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser 465	470	475	1440
gaa gtc acc acc aaa atg ctg tgt gct gac cca cag tgg aaa aca Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr 485	490	495	1488
gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500	505	510	1536
ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515	520	525	1584
ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530	535	540	1632
tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545	550	555	1674

<210> 8  
<211> 591  
<212> DNA  
<213> *Homo sapiens*

<220>

<221> CDS

<222> (1) ... (591)

<223> Coding sequence of the surfactant protein C precursor

<400> 8

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	48
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	96
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtc ctc atc gtc gtg Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	144
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	192
50 55 60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	240
65 70 75 80	
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	288
85 90 95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	336
100 105 110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	384
115 120 125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	432
130 135 140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	480
145 150 155 160	
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	528
165 170 175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	576
180 185 190	
ccg ctc tac tac atc Pro Leu Tyr Tyr Ile	591
195	

<210> 9  
<211> 174  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> CDS  
<222> (1) ... (174)  
<223> Coding sequence of the surfactant protein C precursor lacking the C-terminal propeptide

<400> 9

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccc gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	

tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	

ctg aaa cgc ctt ctt atc gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	

gtg att gtg gga gcc ctg ctc atg ggt ctc	174
Val Ile Val Gly Ala Leu Leu Met Gly Leu	
50 55	

<210> 10  
<211> 105  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (105)  
<223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val	
1 5 10 15	

gtg gtg gtg gtc ctc atc gtc gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu	
20 25 30	

atg ggt ctc	105
Met Gly Leu	
35	

<210> 11  
<211> 1686  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1686)

<223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgc tgc gga Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	48
1 5 10 15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	96
20 25 30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met	144
35 40 45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn	192
50 55 60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser	240
65 70 75 80	
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr	288
85 90 95	
tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu	336
100 105 110	
gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr	384
115 120 125	
gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser	432
130 135 140	
ggc gcc gag tgc acc aac tgg aac agc acg gcg ttg gcc cag aag ccc Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro	480
145 150 160 165	
tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His	528
170 175 180	
aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val	576
185 190 195	
ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys	624
200 205 205	

tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg	210	215	220	672
ggc acg cac agc ctc acc gag tcg ggt gcc tcc tgc ctc ccg tgg aat Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn	225	230	235	240
tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala	245	250	255	768
cag gca ctg ggc ctg ggc aaa cat aat tac tgc cg <sup>g</sup> aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly	260	265	270	816
gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp	275	280	285	864
gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr	290	295	300	912
agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Leu Phe Ala Asp Ile Ala	305	310	315	960
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro	325	330	335	1008
gga gag cg <sup>g</sup> ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile	340	345	350	1056
ctc tct gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu	355	360	365	1104
acg gtg atc ttg ggc aga aca tac cg <sup>g</sup> gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu	370	375	380	1152
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp	385	390	395	400
gac act tac gac aat gac att gc <sup>g</sup> ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser	405	410	415	1200
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro	420	425	430	1248
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly				1296
				1344

435

440

445

tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag 1392  
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
 450 455 460

gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat 1440  
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His  
 465 470 475 480

tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act 1488  
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr  
 485 490 495

cgg agc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat 1536  
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp  
 500 505 510

tcg gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg 1584  
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val  
 515 520 525

ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt 1632  
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly  
 530 535 540

gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg 1680  
 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met  
 545 550 555 560

cga ccg 1686  
 Arg Pro

<210> 12  
<211> 1158  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> sig\_peptide  
<222> (1) ... (69)  
<223> Signal sequence of the surfactant protein B

<220>  
<221> CDS  
<222> (76) ... (312)  
<223> Coding sequence of the mature surfactant protein B

<220>  
<221> CDS  
<222> (313) ... (1140)  
<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>  
<221> CDS  
<222> (1141) ... (1158)  
<223> Hexahistidin affinity tag

<400> 12

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	48
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr	96
20 25 30	
tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro	144
35 40 45	
aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro	192
50 55 60	
ctg gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val	240
65 70 75 80	
atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys	288
85 90 95	
cgc ctc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu	336
100 105 110	
tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile	384
115 120 125	
att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala	432
130 135 140	
atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly	480
145 150 155 160	
agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile	528
165 170 175	
gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg	576
180 185 190	
ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu	624
195 200 205	
atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp	672
210 215 220	

att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro 225 230 235 240	720
tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro 245 250 255	768
cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser 260 265 270	816
acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu 275 280 285	864
att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val 290 295 300	912
acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser 305 310 315 320	960
tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg 325 330 335	1008
atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys 340 345 350	1056
gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile 355 360 365	1104
cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His 370 375 380	1152
cat cat His His 385	1158

<210> 13  
<211> 1149  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> sig\_peptide  
<222> (1) ... (60)  
<223> Signal sequence of the urokinase plasminogen activator  
  
<220>  
<221> CDS  
<222> (67) ... (894)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> CDS

<222> (895) ... (1131)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> CDS

<222> (1132) ... (1149)

<223> Hexahistidin affinity tag

<400> 13

atg	aga	gcc	ctg	ctg	gcg	cgc	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc	48
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser	
1			5					10				15				
gac	tcc	aaa	ggc	agc	aat	aag	ccc	tcc	tct	cct	cca	gaa	gaa	tta	aaa	96
Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Glu	Leu	Lys
20							25					30				
ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag	att	att	ggg	144
Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	
35							40					45				
gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg	gcc	atc	tac	192
Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	
50						55					60					
agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga	ggc	agc	ctc	240
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	
65						70			75			80				
atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc	att	gat	tac	288
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	
85						90						95				
cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	tca	agg	ctt	aac	336
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	
100						105					110					
tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac	ctc	atc	cta	384
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	
115						120					125					
cac	aag	gac	tac	agc	gac	acg	ctt	gct	cac	cac	aac	gac	att	gcc	432	
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	
130						135					140					
ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	tcc	cg	480
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	
145						150				155			160			
act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	gat	ccc	cag	ttt	528
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	
165						170						175				

ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp 180 185 190	576
tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser 195 200 205	624
cac cg <sup>g</sup> gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc His Arg Glu Cys Gln Gln Pro His Tyr Tyr Ser Glu Val Thr Thr 210 215 220	672
aaa atg ctg tgt gct gac cca cag tgg aaa aca gat tcc tgc cag Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln 225 230 235 240	720
gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act Gly Asp Ser Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr 245 250 255	768
ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys 260 265 270	816
cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser 275 280 285	864
cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro 290 295 300	912
tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile 305 310 315 320	960
ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val 325 330 335	1008
cct ctg gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser 340 345 350	1056
gtc atc ctg ctc gac acg ctg ggc cgc atg ctg ccc cag ctg gtc Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val 355 360 365	1104
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His 370 375 380	1149

<210> 14

<211> 381

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (381)

<223> Surfactant protein B precursor

<400> 14

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
145 150 155 160

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
165 170 175

Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
180 185 190

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
195 200 205

Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
210 215 220

Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
225 230 235 240

Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
245 250 255

Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg  
260 265 270

Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro

275

280

285

Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser  
290 295 300

Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala  
305 310 315 320

Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys  
325 330 335

Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg  
340 345 350

Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr  
355 360 365

Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu  
370 375 380

<210> 15

<211> 279

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Surfactant protein B precursor lacking the C-terminal propeptide

<400> 15

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
145 150 155 160

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
165 170 175

Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
180 185 190

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
195 200 205

Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
210 215 220

Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
225 230 235 240

Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
245 250 255

Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg  
260 265 270

Leu Val Leu Arg Cys Ser Met  
275

<210> 16  
<211> 79  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1) ... (79)  
<223> Mature surfactant protein B

<400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys  
1 5 10 15

Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala  
20 25 30

Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys  
35 40 45

Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg  
50 55 60

Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met  
65 70 75

<210> 17  
<211> 431

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (431)

<223> Single-chain urokinase-plasminogen activator

<400> 17

Met Arg Ala Leu Leu Ala Arg Leu Leu Cys Val Leu Val Val Ser  
1 5 10 15

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
20 25 30

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
35 40 45

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
50 55 60

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
65 70 75 80

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
85 90 95

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp  
180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val  
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His  
210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly  
225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val  
245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His

260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys  
275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr  
290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
305 310 315 320

Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val  
325 330 335

Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly  
340 345 350

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys  
355 360 365

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu  
370 375 380

Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys  
385 390 395 400

Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu  
405 410 415

Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
420 425 430

<210> 18

<211> 276

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (276)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 18

Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys  
1 5 10 15

Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
20 25 30

Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly  
35 40 45

Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val  
50 55 60

Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr  
65 70 75 80

Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu  
85 90 95

Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala  
100 105 110

Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser  
115 120 125

Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys  
130 135 140

Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile  
145 150 160

Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln  
165 170 175

(...) Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln  
180 185 190

Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala  
195 200 205

Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro  
210 215 220

Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser  
225 230 235 240

Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg  
245 250 255

Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn  
260 265 270

Gly Leu Ala Leu  
275

<210> 19  
<211> 557  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> PEPTIDE  
<222> (1) ... (279)  
<223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>  
<221> PEPTIDE  
<222> (282) ... (577)  
<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr

1	5	10	15
Leu Cys Gly Pro Gly Thr Ala Ala Trp	Trp Thr Thr Ser Ser Leu Ala Cys		
20	25		30
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln			
35	40		45
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly			
50	55		60
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn			
65	70		75
			80
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu			
85		90	
			95
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys			
100		105	
			110
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln			
115		120	
			125
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys			
130		135	
			140
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu			
145		150	
			155
			160
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu			
165		170	
			175
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His			
180		185	
			190
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195		200	
			205
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210		215	
			220
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225		230	
			235
			240
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245		250	
			255
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260		265	
			270
Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu			
275		280	
			285
Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys			
290		295	
			300
Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala			
305		310	
			315
			320

Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly  
325 330 335

Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe  
340 345 350

Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser  
355 360 365

Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn  
370 375 380

Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn  
385 390 395 400

Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln  
405 410 415

Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp  
420 425 430

Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn  
435 440 445

Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
450 455 460

Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu  
465 470 475 480

Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp  
485 490 495

Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly  
500 505 510

Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu  
515 520 525

Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp  
530 535 540

Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
545 550 555

<210> 20  
<211> 558  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> PEPTIDE  
<222> (1) ... (279)  
<223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>  
<221> PEPTIDE  
<222> (283) ... (558)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
145 150 155 160

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
165 170 175

Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
180 185 190

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
195 200 205

Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
210 215 220

Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
225 230 235 240

Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
245 250 255

Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg  
260 265 270

Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro  
275 280 285

Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe

290

295

300

Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe  
 305                   310                   315                   320

Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys  
 325                   330                   335

Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys  
 340                   345                   350

Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg  
 355                   360                   365

Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu  
 370                   375                   380

Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His  
 385                   390                   395                   400

Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala  
 405                   410                   415

Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn  
 420                   425                   430

Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu  
 435                   440                   445

Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val  
 450                   455                   460

Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser  
 465                   470                   475                   480

Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr  
 485                   490                   495

Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln  
 500                   505                   510

Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala  
 515                   520                   525

Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro  
 530                   535                   540

Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
 545                   550                   555

&lt;210&gt; 21

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1) ... (197)

<223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr  
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His  
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val  
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His  
50 55 60

Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln  
65 70 75 80

Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile  
85 90 95

Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala  
100 105 110

Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro  
115 120 125

Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe  
130 135 140

Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys  
145 150 155 160

Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly  
165 170 175

Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val  
180 185 190

Pro Leu Tyr Tyr Ile  
195

<210> 22

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (58)

<223> Surfactant protein C precursor lacking the C-terminal propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr  
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His  
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val  
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu  
50 55

<210> 23

<211> 35

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (35)

<223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val  
1 5 10 15

Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu  
20 25 30

Met Gly Leu

35

<210> 24

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (562)

<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg  
20 25 30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met  
35 40 45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn  
50 55 60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser  
65 70 75 80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr  
85 90 95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu  
100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr  
115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser  
130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro  
145 150 160 165

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His  
170 175 180

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val  
185 190 195

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys  
200 205 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg  
210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn  
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala  
245 250 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly  
260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp  
275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr  
290 295 300

Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala  
305 310 315 320

Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro  
325 330 335

Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile  
340 345 350

Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu  
355 360 365

Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu  
370 375 380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp  
385 390 395 400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser  
405 410 415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro  
420 425 430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly  
435 440 445

Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
450 455 460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His  
465 470 475 480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr  
485 490 495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp  
500 505 510

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val  
515 520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly  
530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met  
545 550 555 560

Arg Pro

<210> 25  
<211> 386  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> SIGNAL  
<222> (1) ... (23)  
<223> Signal sequence of the surfactant protein B

<220>  
<221> PEPTIDE  
<222> (26) ... (104)  
<223> Mature surfactant protein B

<220>  
<221> PEPTIDE  
<222> (105) ... (380)  
<223> Low molecular weight two-chain urokinase-plasminogen activator

<220>  
<221> PEPTIDE  
<222> (381) ... (386)  
<223> Hexahistidin affinity tag

<400> 25

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr  
20 25 30

Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro  
35 40 45

Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro  
50 55 60

Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val  
65 70 75 80

Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys  
85 90 95

Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu  
100 105 110

Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile  
115 120 125

Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala  
130 135 140

Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly  
145 150 155 160

Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile  
165 170 175

Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg  
180 185 190

Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu  
195 200 205

Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp  
210 215 220

Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro  
225 230 235 240

Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro  
245 250 255

Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser  
260 265 270

Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu  
275 280 285

Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val  
290 295 300

Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser  
305 310 315 320

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg  
325 330 335

Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys  
340 345 350

Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile  
355 360 365

Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His  
370 375 380

His His  
385

<210> 26

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1) ... (20)

<223> Signal sequence of the urokinase plasminogen activator

<220>

<221> PEPTIDE

<222> (23) ... (298)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> PEPTIDE

<222> (299) ... (377)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> PEPTIDE

<222> (378) ... (383)

<223> Hexahistidin affinity tag

<400> 26

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser  
1 5 10 15

Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys  
20 25 30

Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly  
35 40 45

Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr  
50 55 60

Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu

65

70

75

80

Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr  
85 90 95

Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn  
100 105 110

Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu  
           115                   120                   125

His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala  
130 135 140

Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg  
145 150 155 160

Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe  
165 170 175

Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp  
                  180                 185                 190

Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser  
195 200 205

His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr  
210 215 220

Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln  
225 230 235 240

Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr  
                   245                  250                  255

Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys  
260 265 270

Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser  
275 280 285

His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro  
290 295 300

Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile  
 305                    310                    315                    320

Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val  
325 330 335

Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser  
                  340                   345                   350

Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val  
355 360 365

Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His His  
370 . . . . . 375 . . . . . 380 . . . . .

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